## **Listing of Claims:**

This listing of claims replaces all prior versions, and listings, of claims in the captioned application.

- (Original) A computer system comprising at least one database correlating the
  presence of at least one mutation in a human immunodeficiency virus (HIV)
  reverse transcriptase and a change in susceptibility of at least one strain of HIV to
  a reverse transcriptase inhibitor, comprising at least one record corresponding to a
  correlation between at least one mutation 194G in said reverse transcriptase, and
  treatment with at least a reverse transcriptase inhibitor.
- 2. (Original) A method for evaluating the effectiveness of a reverse transcriptase inhibitor as an antiviral therapy for a patient infected with at least one mutant HIV straincomprising:
  - (i) collecting a sample from an HIV-infected patient;
  - (ii) determining whether the sample comprises a nucleic acid encoding HIV reverse transcriptase having at least one mutation 194G;
  - (iii) correlating the presence of said at least one mutation of step (ii) to a change in effectiveness of said reverse transcriptase inhibitor.
- 3. (Original) A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:
  - (i) providing a HIV reverse transcriptase nucleic acid comprising at least one mutation 194G;
  - (ii) recombining said nucleic acid of step (i) into a proviral nucleic acid deleted for said sequence to generate a recombinant HIV virus;
  - (iii) determining a phenotypic response of said drug to said HIV reverse transcriptase; and
  - (iv) identifying a drug effective against mutant HIV based on the phenotypic response of step (iii).
- 4. (Original) A method for identifying a drug effective against mutant HIV reverse transcriptase, comprising:

- (i) providing a HIV reverse transcriptase comprising at least one mutation 194G;
- (ii) determining the activity of said drug on said HIV reverse transcriptase;
- (iii) determining the activity of said drug on wild type HIV reverse transcriptase;
- (iv) determining the ratio of the activity determined in step (iii) over the activity determined in step (ii);
- (v) identifying an effective drug against mutant HIV based on the ratio of step (iv).
- (Original) A method for evaluating a change in viral drug susceptibility comprising:
  - (i) collecting a sample from an HIV-infected patient;
  - (ii) determining whether the sample comprises a HIV reverse transcriptase having at least one mutation 194G;
  - (iii) correlating the presence of said at least one mutation of step (ii) to a change in viral drug susceptibility.
- 6. (Original) A method for evaluating a change in viral drug susceptibility, comprising:
  - (i) providing an HIV comprising a reverse transcriptase comprising at least one mutation 194G;
  - (ii) determining a phenotypic response of said virus to said drug; and
  - (iii) correlating the phenotypic response of step (ii) to a change in viral drug susceptibility.
- 7. (Original) A method for evaluating a change in drug effectiveness against mutant HIV reverse transcriptase, comprising:
  - (i) providing a HIV reverse transcriptase comprising at least one mutation 194G;
  - (ii) determining the activity of said drug on said reverse transciptase;
  - (iii) determining the activity of said drug on wild type HIV reverse transcriptase and;
  - (iv) determining the ratio of the activity determined in step (iii) over the activity determined in step (ii);

- (v) identifying an effective drug against mutant HIV based on the ratio of step (iv).
- 8. (Original) A vector for performing phenotypic analysis comprising an HIV sequence having at least one mutation 194G in the HIV reverse transcriptase.
- 9. (Original) An isolated and purified HIV reverse transcriptase sequence having at least one mutation 194G, wherein said at least one mutation in said sequence correlates to a fold change in susceptibility towards a HIV reverse transcriptase inhibitor.
- 10. (Original) An isolated and purified oligonucleotide comprising a HIV reverse transcriptase sequence of 5 to 100 bases for in vitro diagnosis of viral drug resistance, characterized in that said oligonucleotide comprises at least one mutation 194G.